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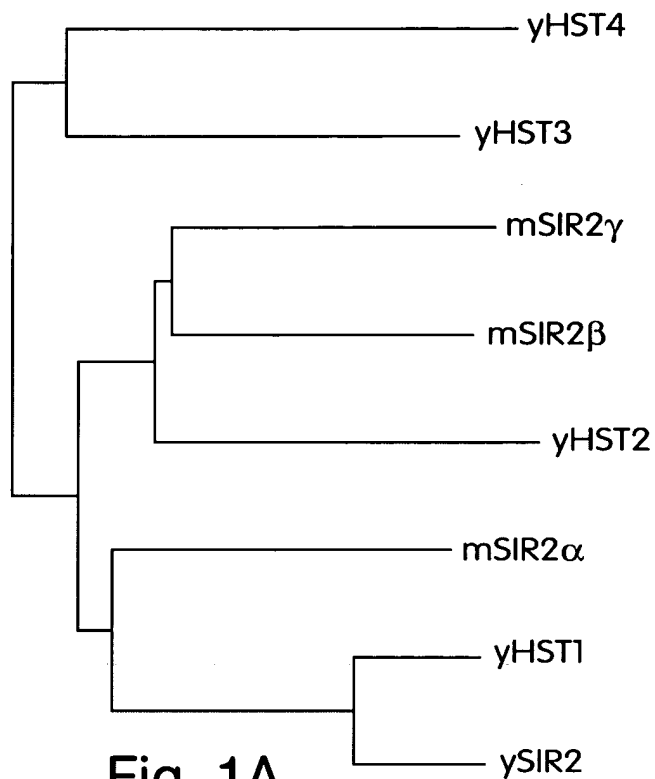
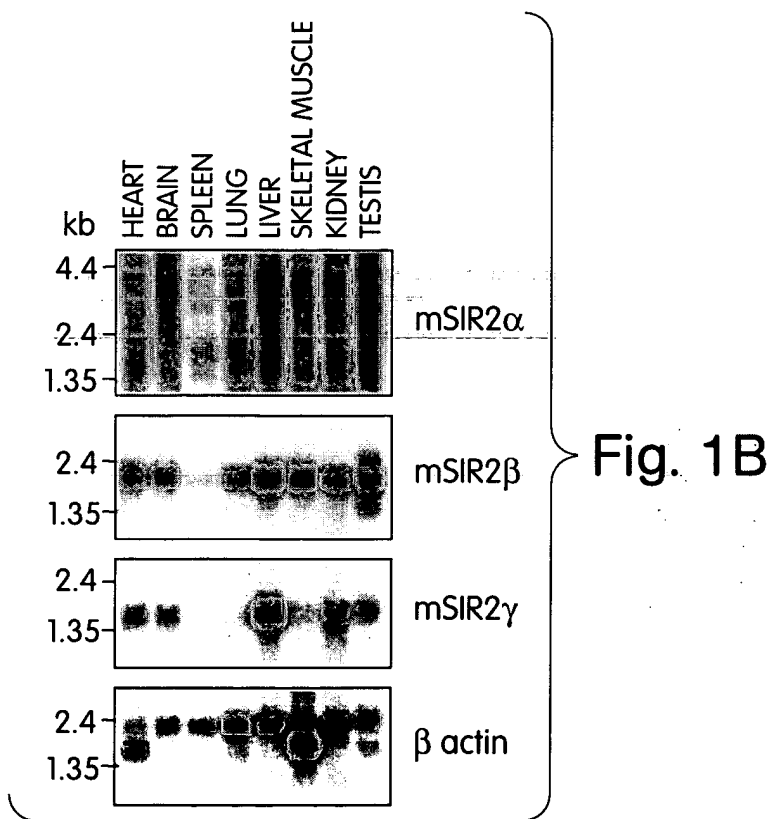


Fig. 1A





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1 MADEVALALQAAGSPSAAAAMEAASQPADEPLRKRPRRDG
41 PGLGRSPGEPSSAAVAPAAAGCEAASAAAPAAALWREAAGAA
81 ASAEREAPATAVAGDGDNGSGLRREPRAADDFFDDDEGEEE
121 DEAAAAAAAAAAIGYRDNLLLTGGLLTNGFHSCESDDDDR
161 SHASSSDWTTPRPRIGPYTFVQQHLMIGTDPRTILKDLLPE
201 TIPPELDDMTLWQIVINILSEPPKRKKRKRDINTIEDAVK
241 LLQECKKIIVLTGAGVSVSCGIPDFRSRDGIYARLAVDFP
281 DLPDPQAMFDIEYFRKDPRPFFKFAKEIYPGQFQPSLCHK
321 FIALSDKEGKLLRNYTQNI DTLEQVAGIQRILQCHGSFAT
361 ASCLICKYKVDCEAVRGDIFNQVVP RCP RCPADEPLAIMK
401 PEIVFFGENLPEQFHAMKYDKDEVDLLIVIGSSLKVRPV
441 ALIPSSIPHEVPQILINREPLPHLHFDVELLGD CDVIINE
481 LCHRLGGEYAKLCCNPVKLSEITEKPPRPQKELVHLSELP
521 PTPHISEDSSSPERTVPQDSSVIATLVDQATNNNVNDLE
561 VSESSCVEEK PQEVQTSRNVENINVENPDFKAVGSSTADK
601 NERTSVAETVRKCWPNRLAKEQISKRLGNQYLFVPPNRY
641 IFHGAEVYSDESDDVLSSSSSCGSNSDSGTCQSPSLEEPL
681 DESEIEEFYNGLEDDTERPECAGGSGFGADGGDQEVVNEA
721 IATRQELTDVNYP SDKS

Fig. 2A

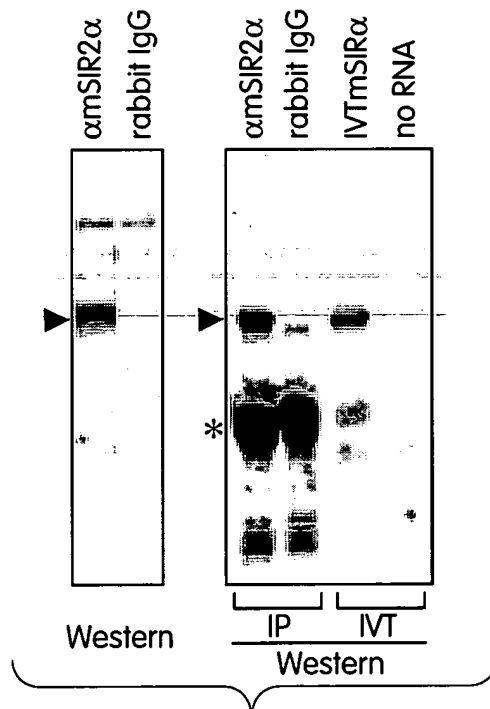


Fig. 2B



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ySIR2	1	IN KVLCT --- RLRLSNFFFTIDHFIQKLH TARKI	30
yHST1	1	IN KVLST --- RLRLPNFNTIDHFTATLRNAKKI	30
mSIR2 α	1	VINILSEPPKRKKRKDINTIEDAKKLQECKKI	33
CobB	1	-----MMENPRV	7
ySIR2	31	LVL TGAGVSTSLGIPDFRSSEGEYS - KIKHLG	61
yHST1	31	LVL TGAGVSTSLGIPDFRSSEGEYS - KIRHLG	61
mSIR2 α	34	IVLTGAGVSVSCGIPDFRSRDGIYARLAVDFPD	66
CobB	8	LVL TGAGISAESGIRTFRAADGLWE - EHRVED	38
ySIR2	62	LDDPODVFNYNIFMHDPVSFYNTIANMVLP - PEK	93
yHST1	62	LEDPODVFNLDIFLQDPVSFYNTIAHNVLP - PEN	93
mSIR2 α	67	LPDPOAMEDIEYERKDPPEFKFAKEIYP - GQF	98
CobB	39	VATPEGFARNPGLVOT - - - EYNARRQQLQOPEI	68
ySIR2	94	IYSPLHSFIKMLQM - KGKLLRNYTONIDNLESY	125
yHST1	94	MYSPLHSFIKMLQD - KGKLLRNYTONIDNLESY	125
mSIR2 α	99	QPSLCHKFIALS DK - EGKLLRNYTONIDTLEQV	130
CobB	69	QPNAAHLALANLKKRLAIAFLLVTONIDNLHER	101
ySIR2	126	AGISTDKLVQCHGSFATATCVTCHWNLPGERTF	158
yHST1	126	AGIDPKLVQCHGSFATASCVTCHWQIPGEKTF	158
mSIR2 α	131	AGIQ - - RIQCHGSFATASCLICKYKVDCBAVR	161
CobB	102	AGNR - - NIQMHGELLKVRCSQSQGLEWNGDV	132
ySIR2	159	NKIRNLELPLCPYCYKKRREYFPEGYNNKV GVA	191
yHST1	159	ENIRNLELPLCPYCYQKRKQYFPM SNGNNT - - -	188
mSIR2 α	162	GDI FNQVVRCPRC - - - - - P - - - - -	176
CobB	133	MPEDKCHC CQFPAPLRPHVVWEG - EMP - - - - -	158
ySIR2	192	ASQGSMSERPPVILNSYGVLPKPDITFFGEALPN	224
yHST1	189	- VQTNINFN SP - ILKSYGVLPKPDITFFGEALPS	219
mSIR2 α	177	- - - - - A - - DEP - - - - - LAIMKPEIVFFGENLPE	197
CobB	159	- - - - - LGMDEIYMA L SMADI FIAIGTS GHVYPA	186
ySIR2	225	K - - FHK SIRE DILECDLLIC - - - TGTSLKVAPV	252
yHST1	220	R - - FHK TIRKDILECDLLIC - - - TGTSLKVAPV	247
mSIR2 α	198	Q - - FHRAMKYDKDEV DLLIV - - - TGS SLKVRPV	225
CobB	187	AGFVHEAKLHGAHTVELNLEPSQVGN EFEEKHY	219
ySIR2	253	SEIVNMVPSHVPOVLINRDP	272
yHST1	248	SEIVNMVPSHVPOVLINRDM	267
mSIR2 α	226	ALIPSSIPHEVPOVLINREP	245
CobB	220	GPASQVVRPEFVDKELKGL - -	237

Fig. 2C



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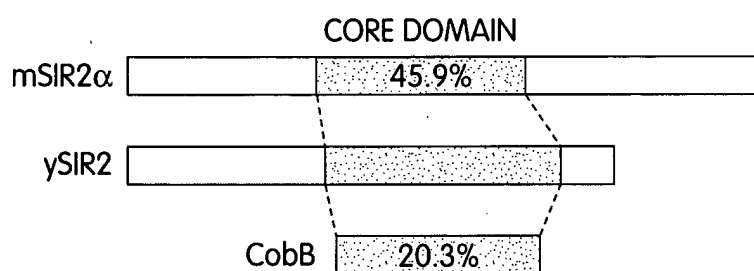


Fig. 2D

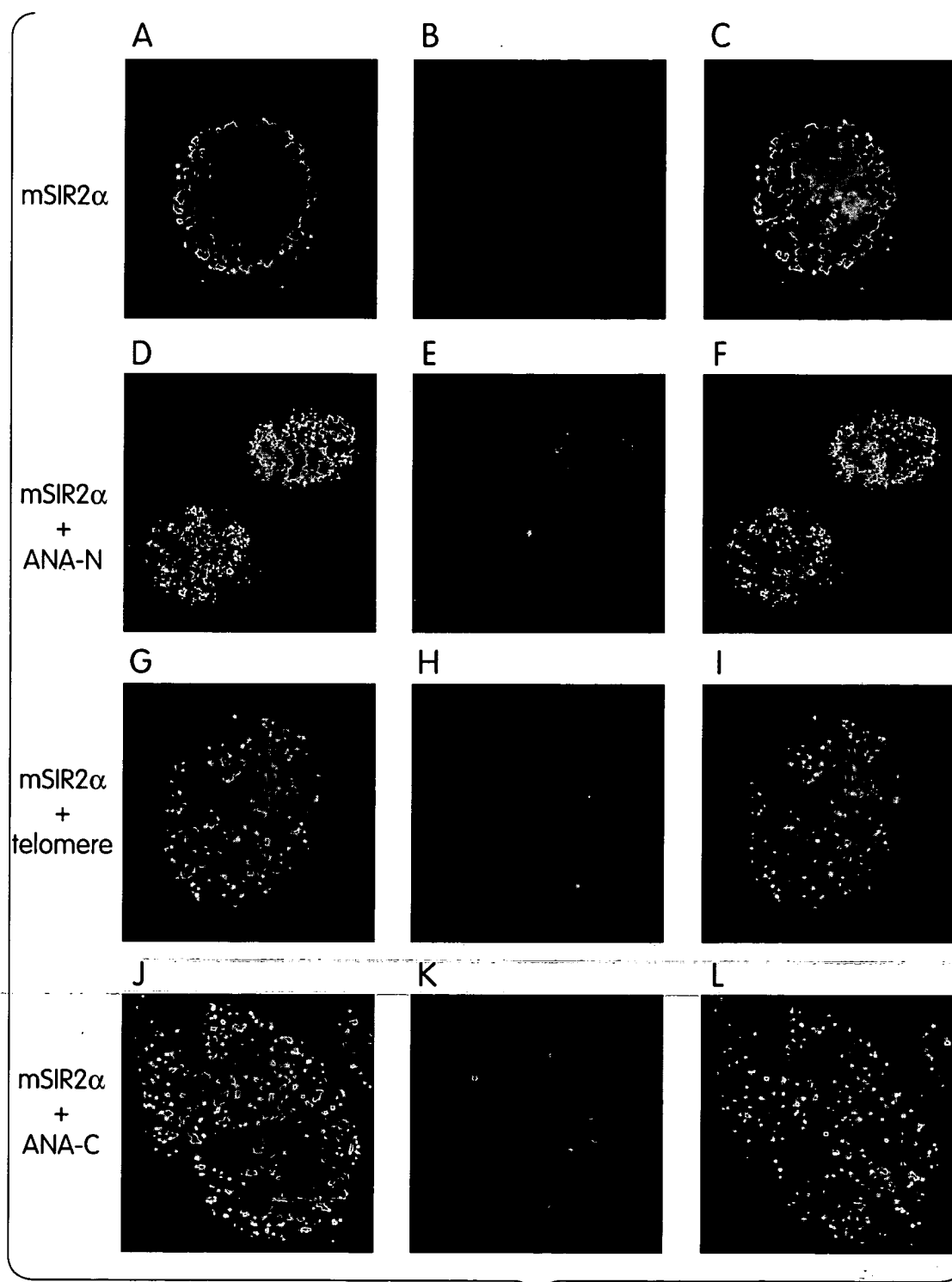


Fig. 3

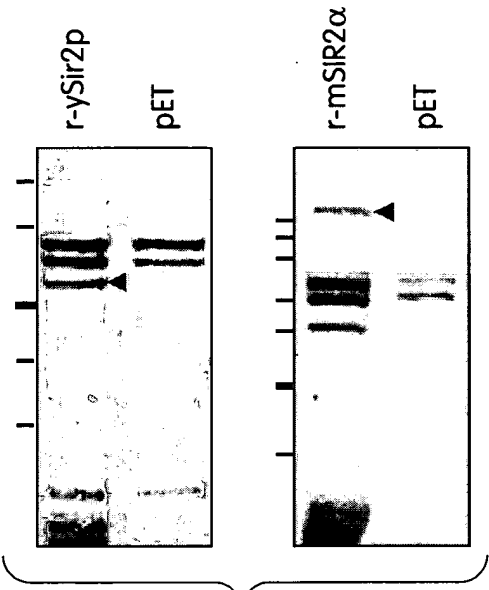


Fig. 4A

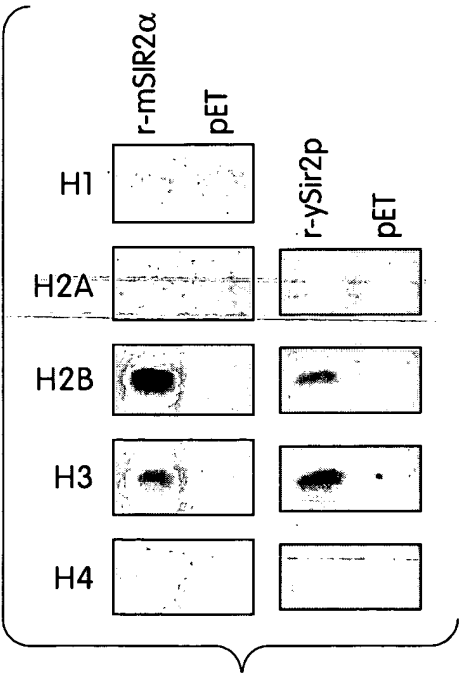


Fig. 4B



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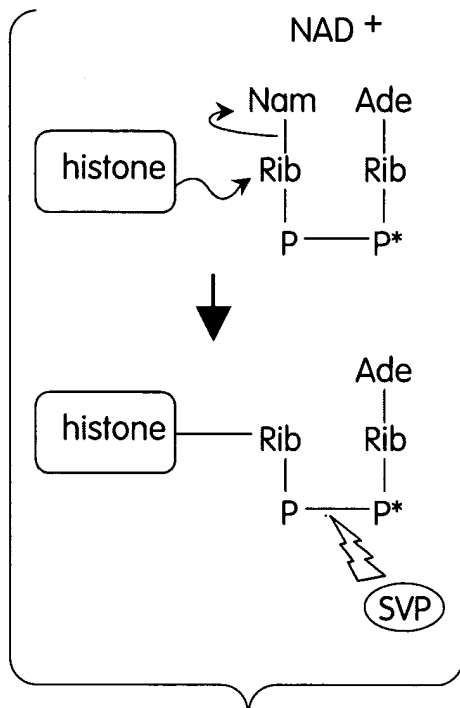


Fig. 4C



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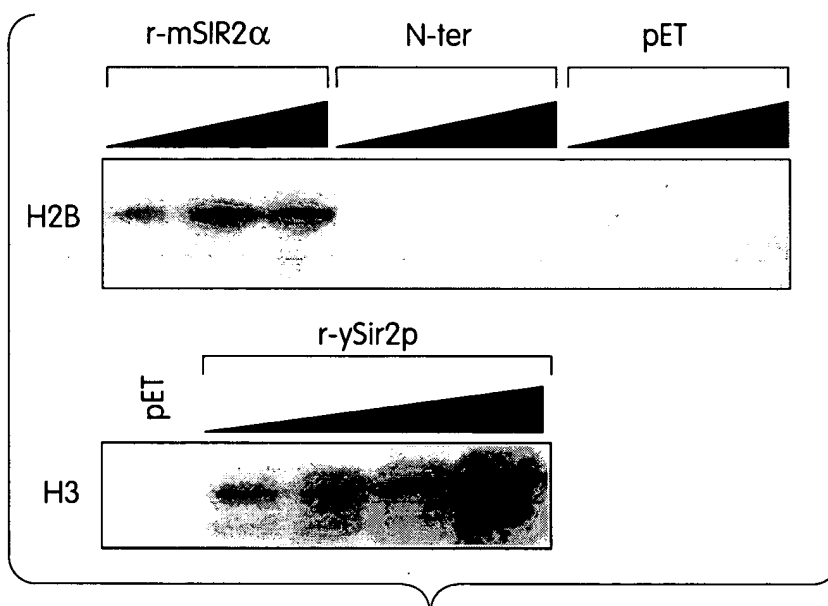


Fig. 4D

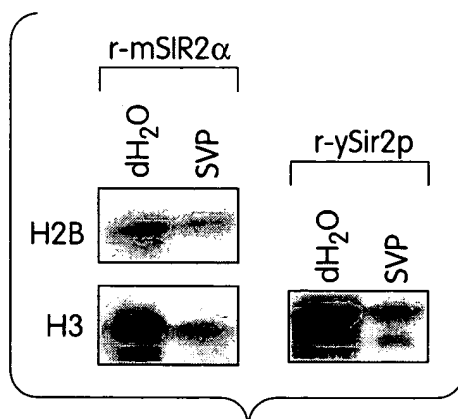


Fig. 4E



Fig. 4F

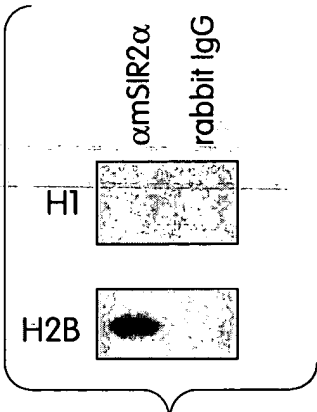


Fig. 4G

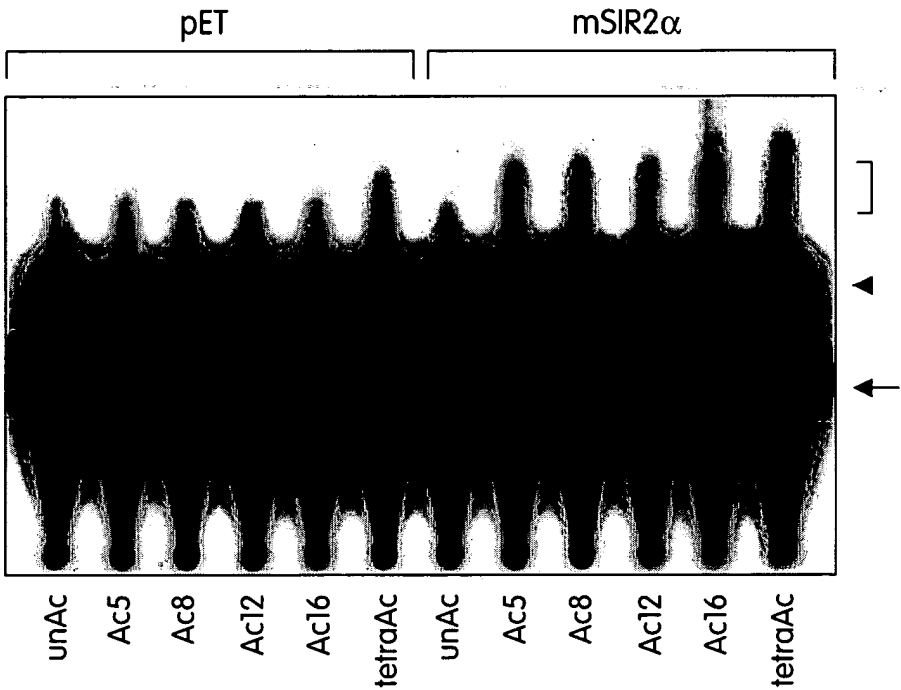


Fig. 5C

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mSIR2 α	249	I	V	L	T	G	A	G	V	S	V	S	C	G	I	P	D	F	R	S	R	D	G	I	Y	A	R	L	A	V	D	F	P	D
ySIR2	258	L	V	L	T	G	A	G	V	S	T	S	L	G	I	P	D	F	R	S	S	E	G	F	Y	S	-	-	K	I	K	H	L	G

mSIR2 α	282	L	P	D	P	Q	A	M	F	D	I	E	Y	F	R	K	D	P	R	P	F	F	K	F	A	K	E	I	Y	P	-	G	Q	F
ySIR2	289	L	D	D	P	Q	D	V	F	N	Y	N	I	F	M	H	D	P	S	V	F	Y	N	I	A	N	M	V	L	P	-	P	E	K

mSIR2 α	314	Q	P	S	L	C	H	K	F	I	A	L	S	D	K	-	E	G	K	L	R	N	Y	T	Q	N	I	D	T	L	E	Q	V
ySIR2	321	I	Y	S	P	L	H	S	F	I	K	M	L	Q	M	-	K	G	K	L	R	N	Y	T	Q	N	I	D	N	L	E	S	Y

mSIR2 α	346	A	G	I	Q	-	-	R	I	L	Q	C	H	G	S	F	A	T	A	S	C	L	I	C	K	Y	K	V	D	C	E	A	V	R
ySIR2	353	A	G	I	S	T	D	K	L	V	Q	C	H	G	S	F	A	T	A	T	C	V	T	C	H	W	N	L	P	G	E	R	I	F

Fig. 6A

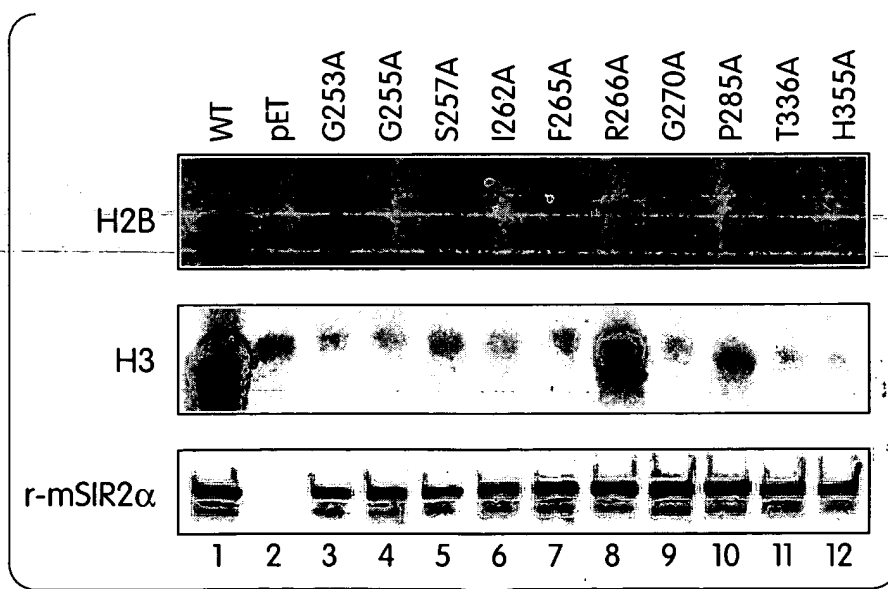
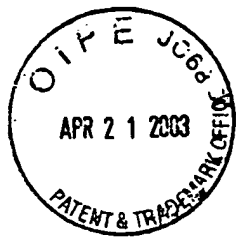


Fig. 6B



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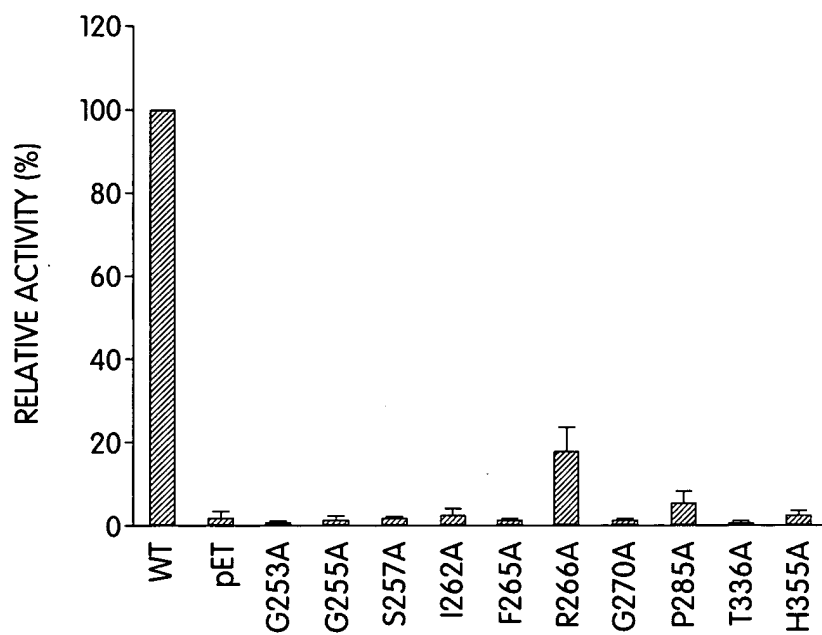


Fig. 6C

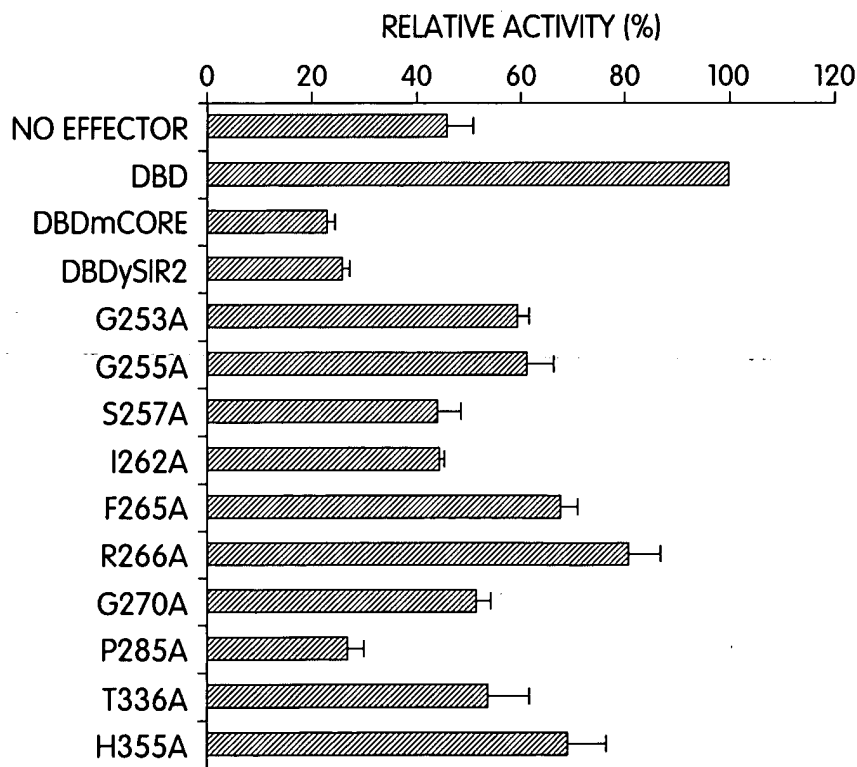


Fig. 6D

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Active Chromatin

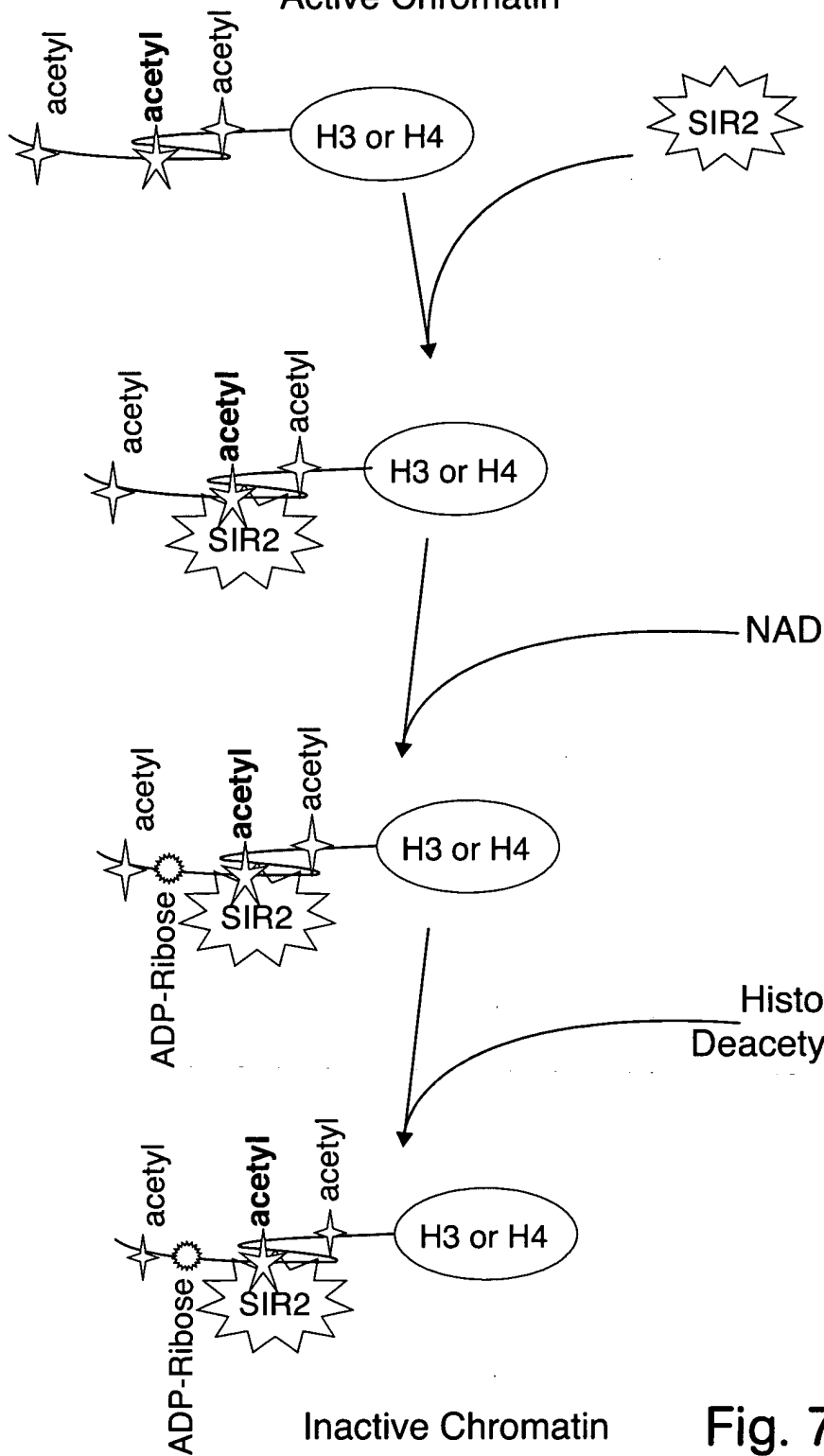
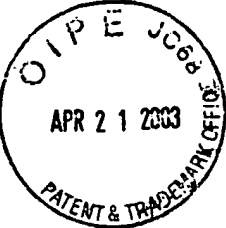


Fig. 7



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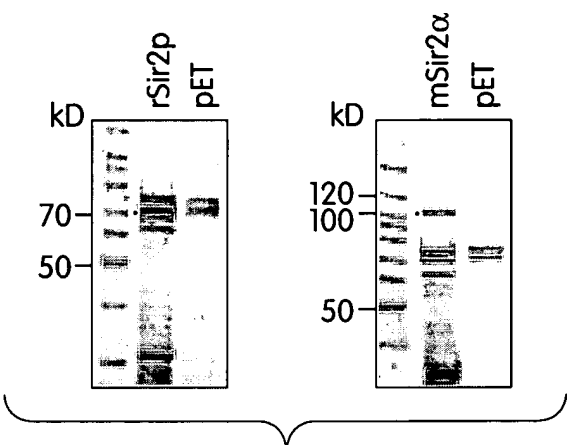


Fig. 8A

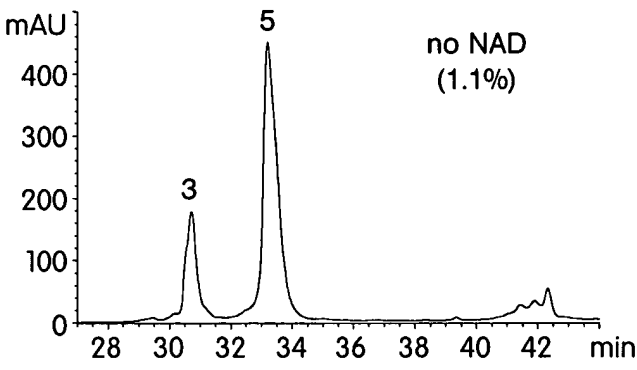


Fig. 8B

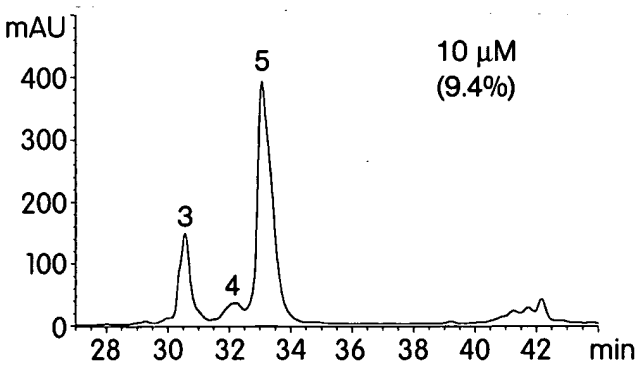


Fig. 8C



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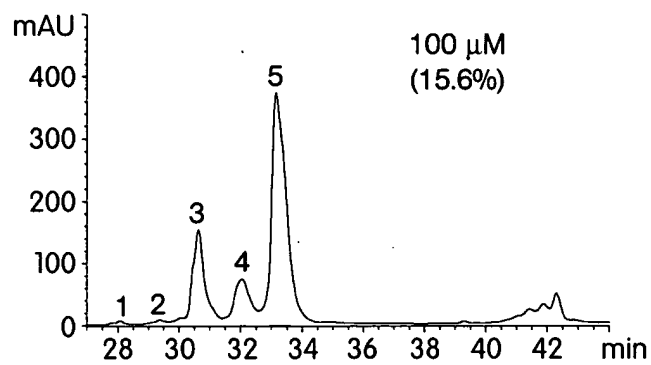


Fig. 8D

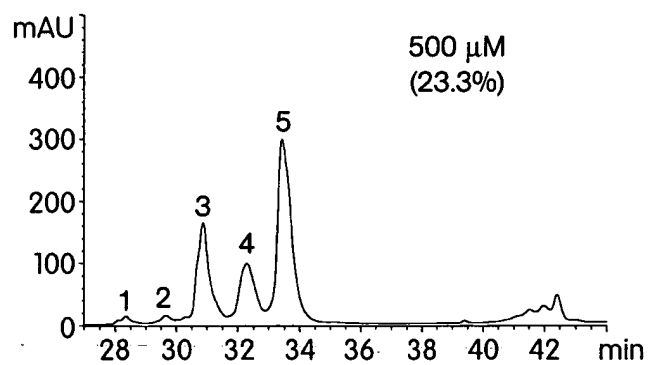


Fig. 8E



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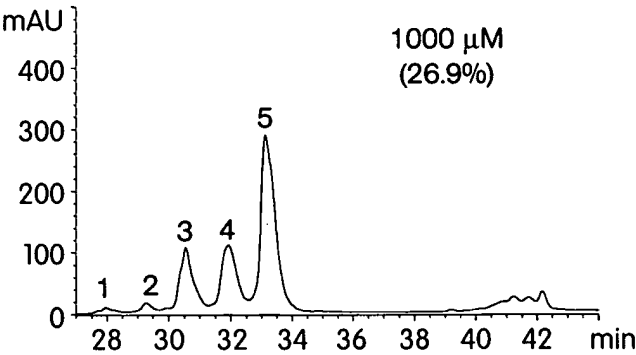


Fig. 8F

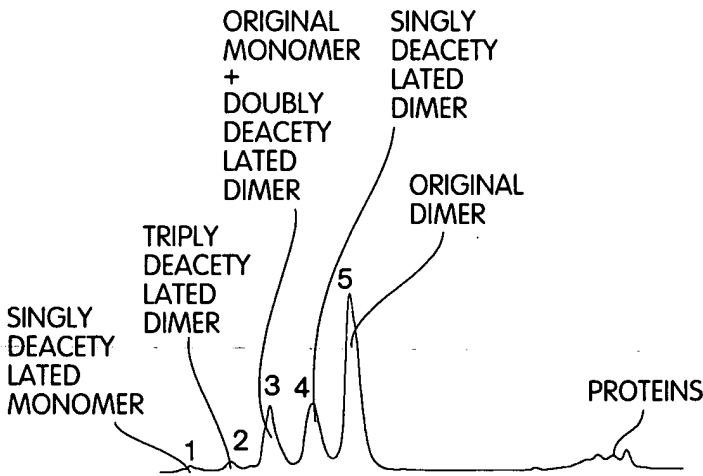


Fig. 8G



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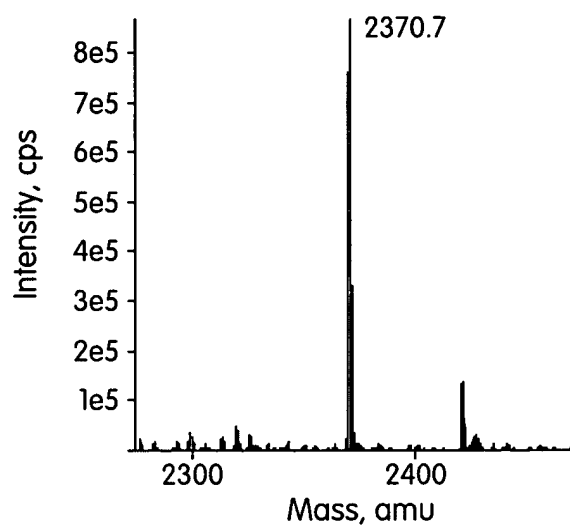


Fig. 9A

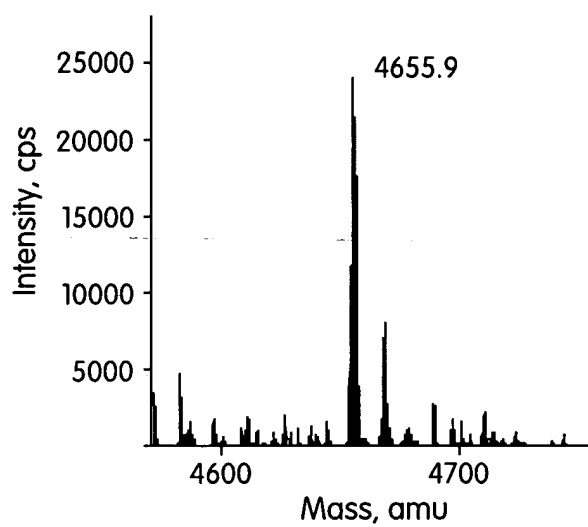
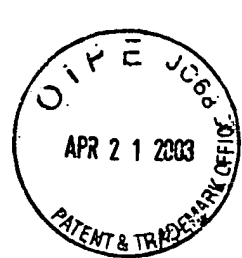


Fig. 9B



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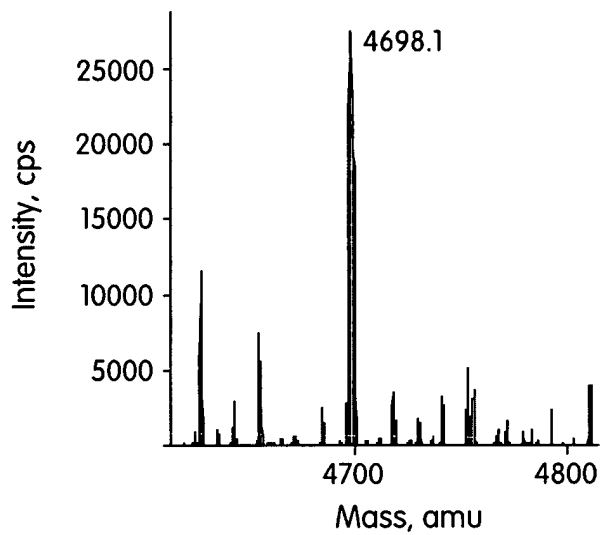


Fig. 9C

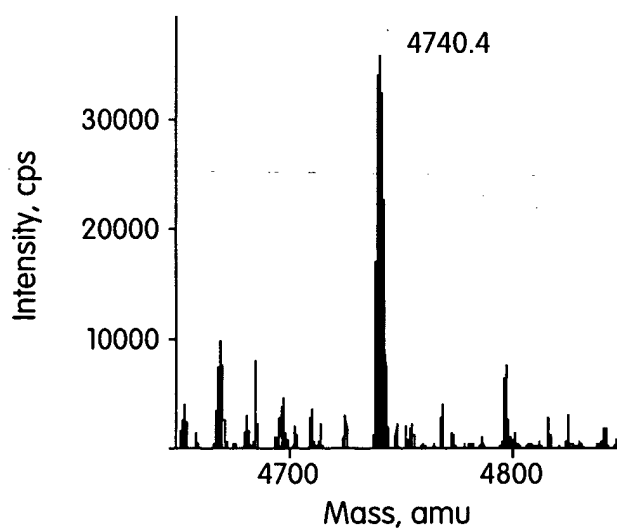
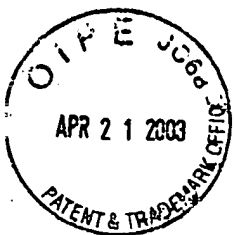


Fig. 9D



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peak 4

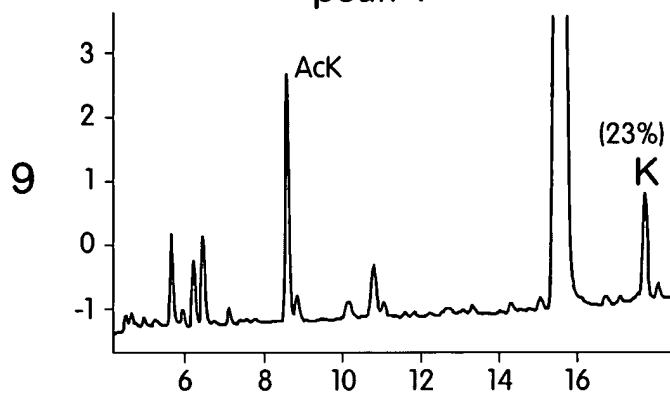


Fig. 10A

peak 4

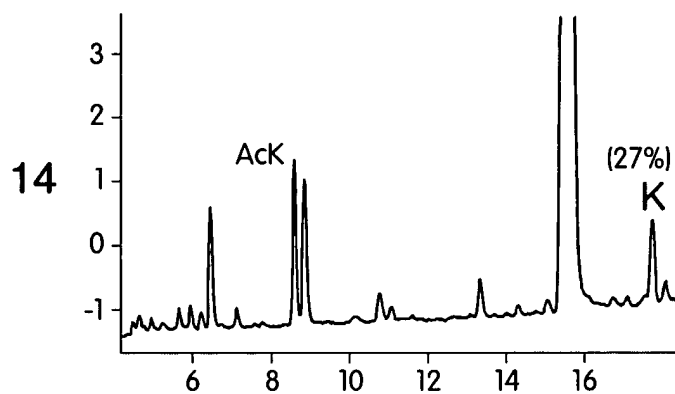


Fig. 10B

peak 4

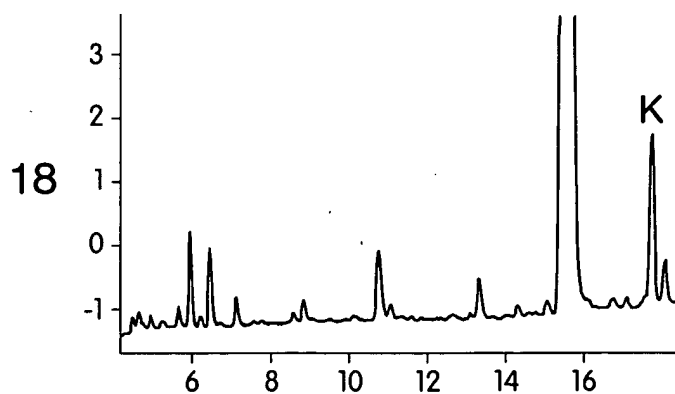


Fig. 10C



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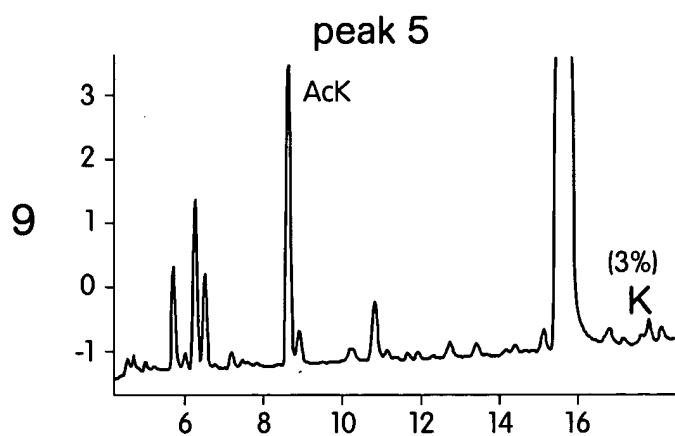


Fig. 10D

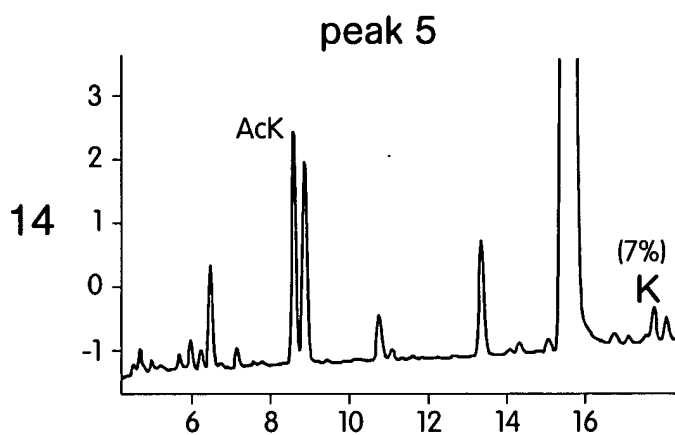


Fig. 10E

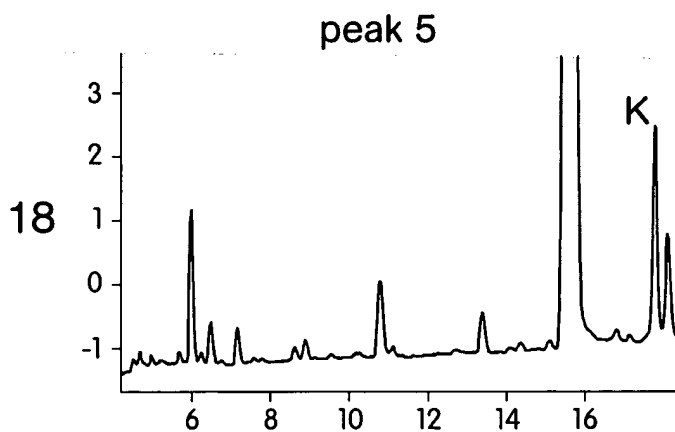


Fig. 10F



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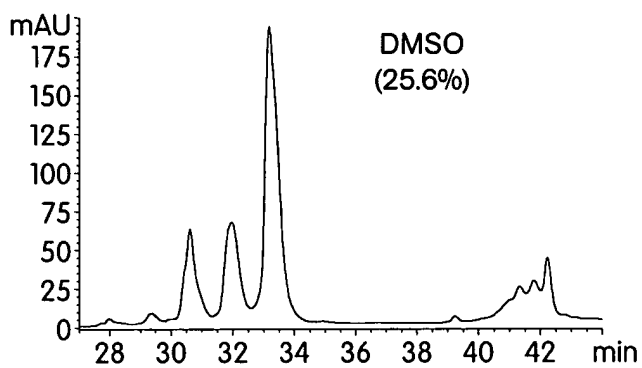


Fig. 11A

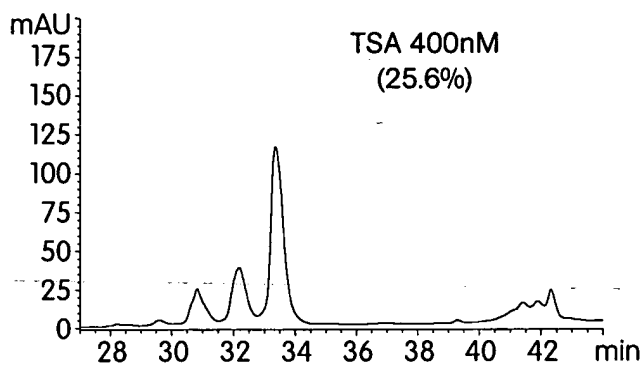


Fig. 11B

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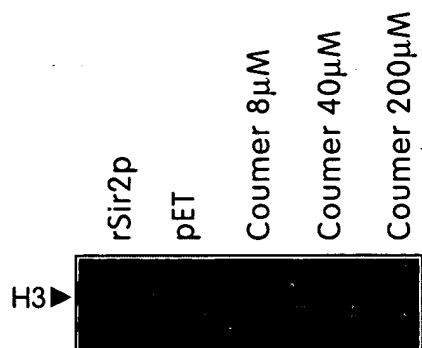


Fig. 11C

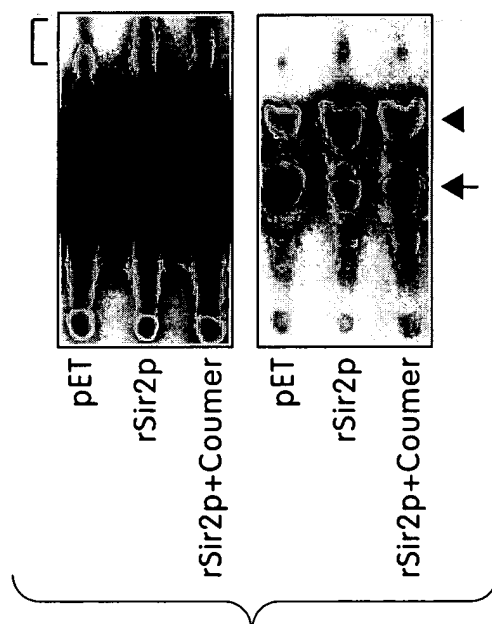


Fig. 11D

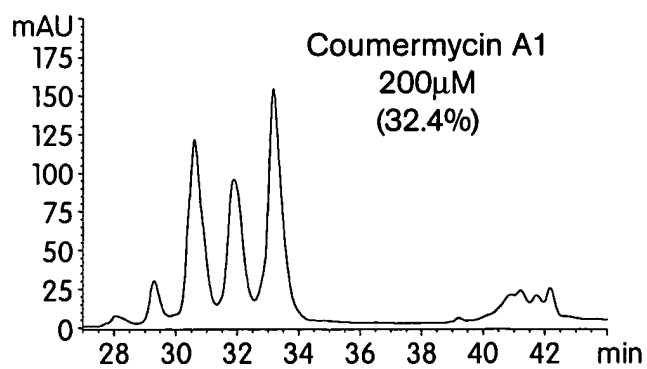
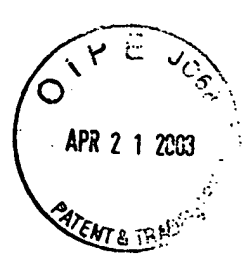


Fig. 11E



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1 MADEVALALQAAGSPSAAAAMEAASQPADEPLRKRPRRDG
41 PGLGRSPGEPSSAAVAPAAAGCEAASAAAPAALWREAAGAA
81 ASAEREAPATAVAGDGDNGSGLRREPRAADDFDDDEGEEE
121 DEAAAAAAAAAIGYRDNLLLTGLLTNGFHSCESDDDDDRT
161 SHASSSDWTTPRPRIGPYTFVQQHLMIGTDPRTILKDLLPE
201 TIPPELDDMTLWQIVINILSEPPKRKKRKDINTIEDAVK
241 LLQECKKIIVLTGAGVSVSCGIPDFRSRDGIYARLAVDFP
281 DLPDPQAMFDIEYFRKDRPFKFKEIYPGQFQPSLCHK
321 FIALSDKEGKLLRNYTQNI DTLEQVAGIQRILQCHGSFAT
361 ASCLICKYKVDCEAVRGDIFNQVVPRCPRCPADEPLAIMK
401 PEIVFFGENLPEQFHRAMKYDKDEVDLLIVIGSSLKVRPV
441 ALIPSSIPHEVPQILINREP LPHLHFDVELLGDCDVIINE
481 LCHRLGGEYAKLCCNPVKLSEITEKPPRPQKELVHLSELP
521 PTPHISEDSSSPERTVPQDSSVIATLVDQATNNNVNDLE
561 VSESSCVEEKPEVQTSRNVENINVENPDFKAVGSSTADK
601 NERTSVAETVRKCWPNRLAKEQISKRLGNQYLFVPPNRY
641 IFHGAEVYSDSEDDVLSSSSSCGSNSDSGTCQSPSLEEPL
681 DESEIEEFYNGLEDDTERPECAGGSGFGADGGDQEVVNEA
721 IATRQELTDVNYPSDKS

Fig. 12A



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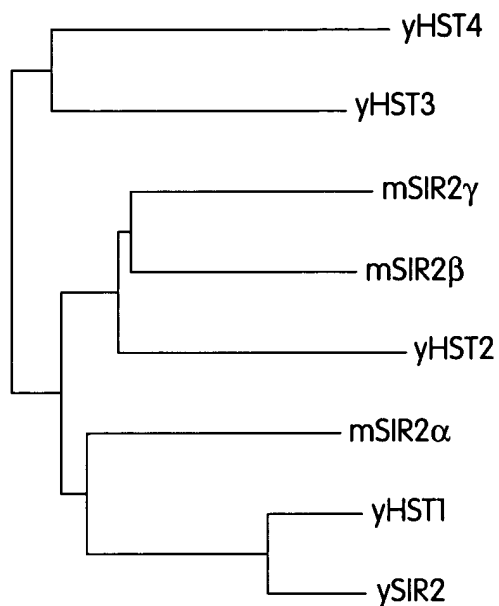


Fig. 12B

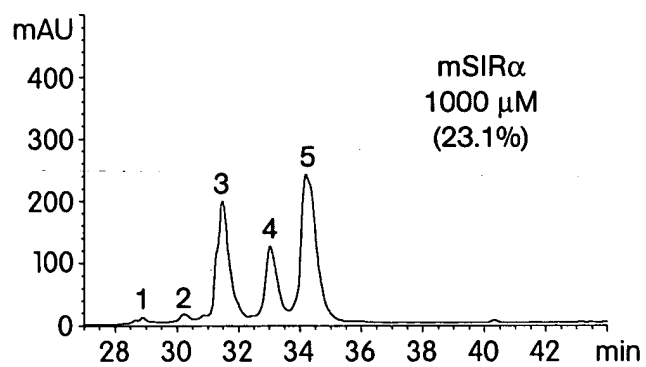


Fig. 12C



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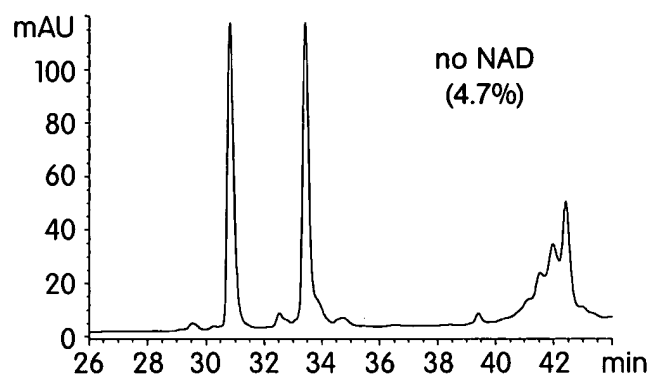


Fig. 13A

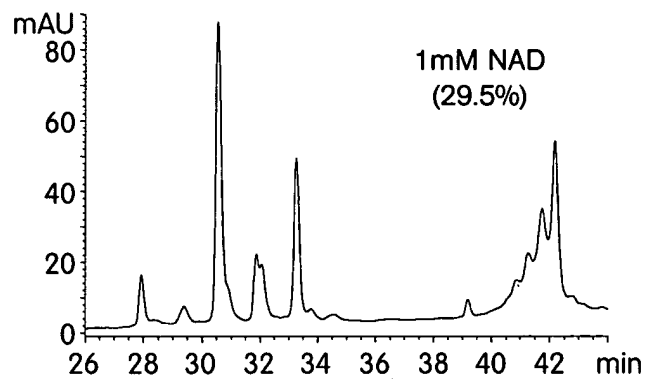


Fig. 13B

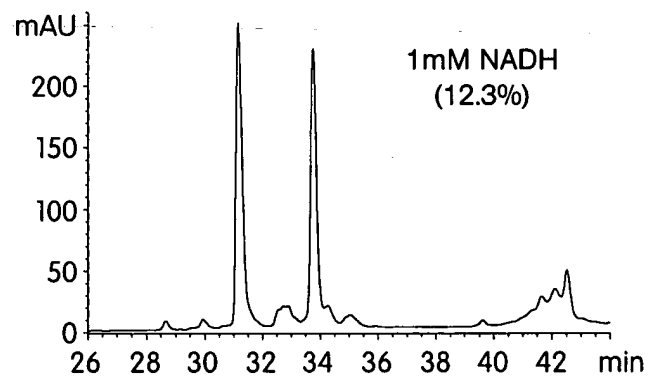


Fig. 13C



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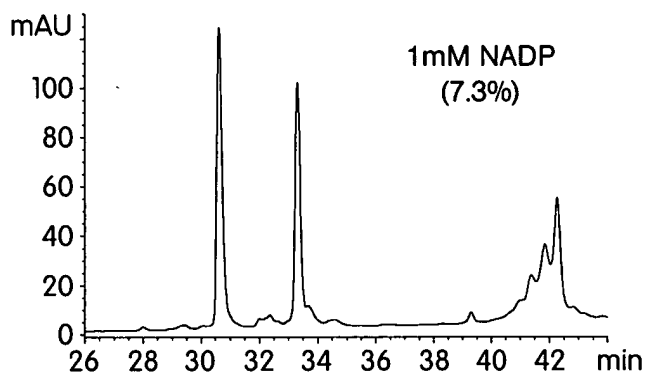


Fig. 13D

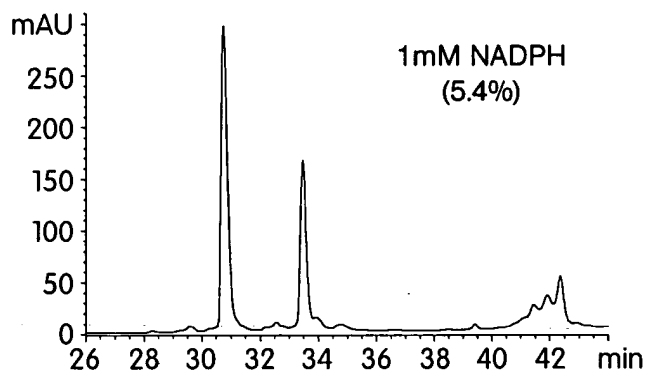


Fig. 13E



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ySIR2	227	AINKVLCT--RLRLSNFFTTIDHFTQKLEHTARKI	257
mSIR2 α	231	VINILSEPPKRRKKRKTINTIEDAVKLLQECKKI	263
CobB	1	-----MMENPRV	7
<div>▼▼▼</div>			
ySIR2	258	LVLTGAGVSTSLGIPDFRSSEGFYSKTKHLG--	288
mSIR2 α	264	LVLTGAGVSVSCGIPDFRSRDGIYARLAVDFPD	296
CobB	8	LVLTGAGISAEESGIRTFRAADGLWEEHRVED--	38
<div>▼▼</div>			
ySIR2	289	EDDPQDVFNYNIFMHDPSVFYNTANMVLPPEKI	321
mSIR2 α	297	LPDPQAMFDIEYFRKDPRPFFKFAKETYPGQFQ	329
CobB	39	VATPEGFARNPGLVOT--EYNARROQLQOPEIQ	89
<div>▼▼</div>			
ySIR2	322	VSPLHSFTKMLQM-EKGLLRNYTONTIDNLESYA	353
mSIR2 α	330	PSLCHKFIALSDEK-EKGLLRNYTONTIDTLEQVA	361
CobB	70	PNAHLALANLKKRLATAELLVTONTIDNLHERA	102
<div>▼▼</div>			
ySIR2	354	GTSTDKLVQCHGSFATATCTVCHWNLPGERIFN	386
mSIR2 α	362	GIQ--RILOCHGSFATASCLICKYKVDCEAVRG	392
CobB	103	GNR--NTTOMHGELLKVRCSQSGQILEWN--G	130
<div>▼▼</div>			
ySIR2	387	KIRN-LELPLCPYCYKKRREYFPEGYNKVGVA	418
mSIR2 α	393	DIFN-QVVRCPRCPP-----	406
CobB	131	DVMP---EDKCHCCQ-----	142
<div>▼▼</div>			
ySIR2	419	ASQGSMSERPPYILNSYGVLPDITFFGEALPN	451
mSIR2 α	407	-----ADEP-----LAIMKPEIVFFGENLPE	427
CobB	143	-----FPAP-----L---RPHVVMFEGEMP--	158
<div>▼▼</div>			
ySIR2	452	KPHKSTREDILECDLLICIGTSLKVAPVS-EIV	483
mSIR2 α	428	QFHRAMKYDKDEVDLLIVIGSSSLKVRPVA-LIP	459
CobB	159	LGMDEITYMALSMADIFIAIGTSGHVYPAAAGFVH	191
<div>▼▼</div>			
ySIR2	484	NMVP SHVPOVLTNHDP-VKHAFFDLSLLGYCD	515
mSIR2 α	460	SSIPHEVPOILINREP-LPHLHFDVELLGDCDV	491
CobB	192	EAKLHGAHTVELNLEPSQVGNEFEKHYGPASQ	224
<div>▼▼</div>			
ySIR2	516	TAAMVAOKCGWTIPHKKWMDLKNKNEKCKQEKDK	548
mSIR2 α	492	TINELCHRLGGEYAKLCCMPVKLSEITEKPPRP	524
CobB	225	VVPEFVDKFLKGL-----	237
<div>▼▼</div>			
ySIR2	549	GVYVVTSDDEHPKTL-----	562
mSIR2 α	525	QKELVHLSELPPPLPHISEDSSSPERTVPQDSS	557
CobB	0	-----	237

Fig. 14A

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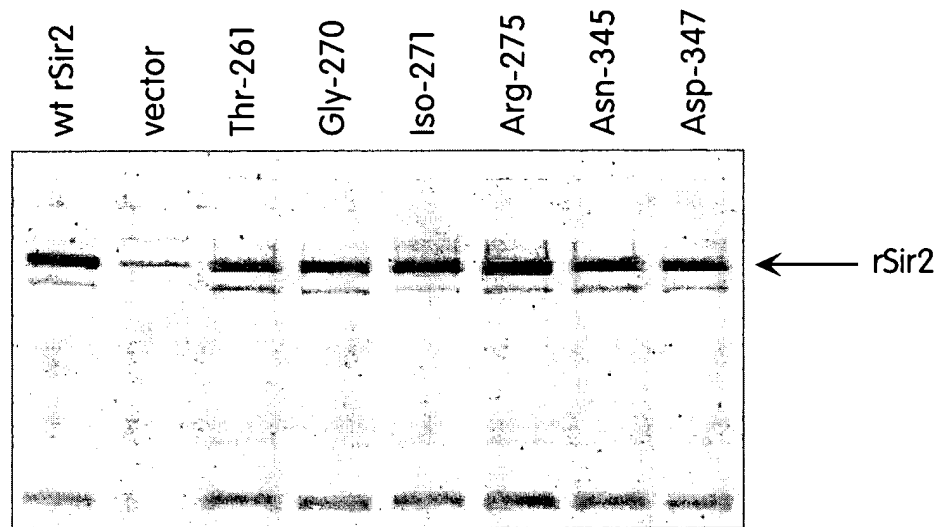


Fig. 14B

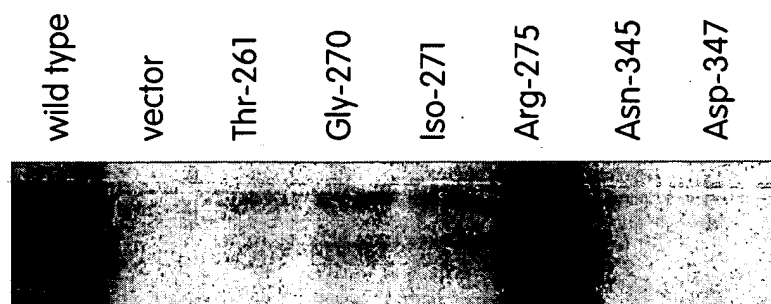


Fig. 14C



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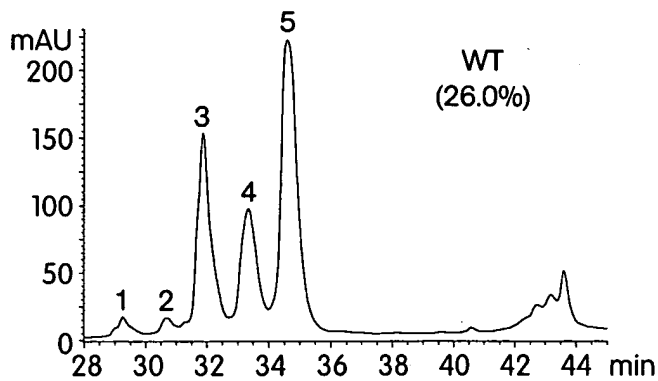


Fig. 15A

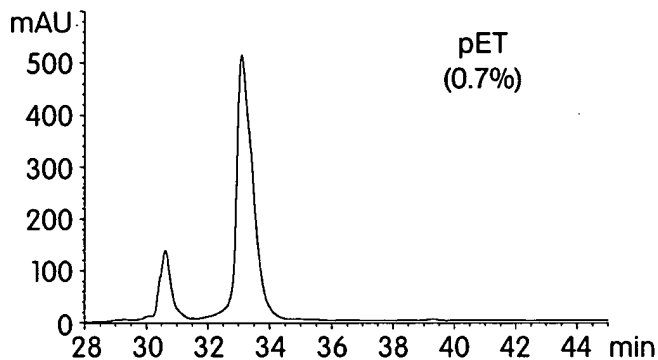


Fig. 15B

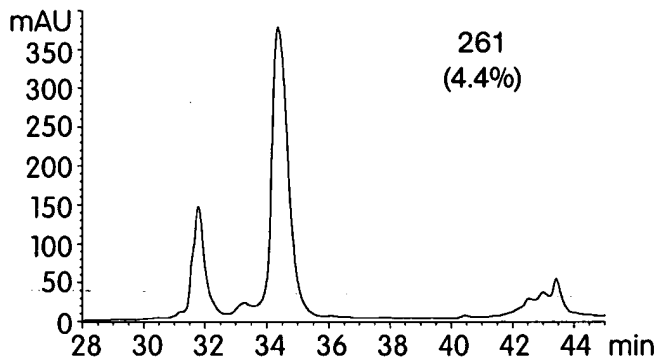


Fig. 15C

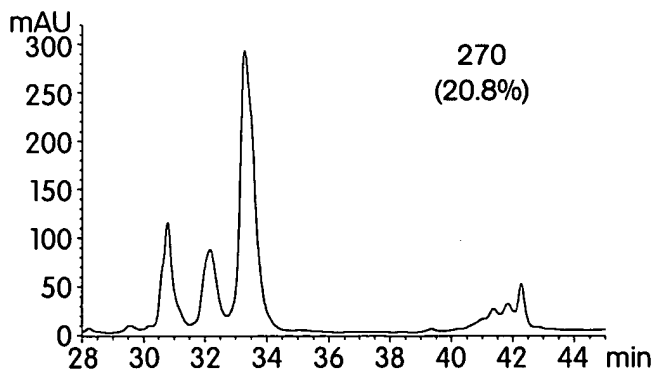
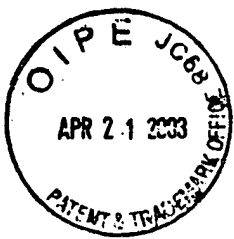


Fig. 15D



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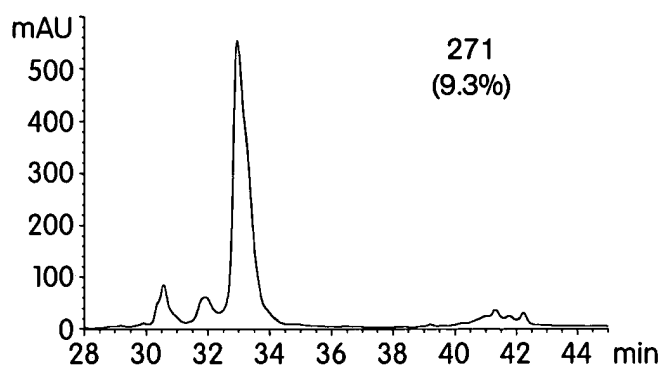


Fig. 15E

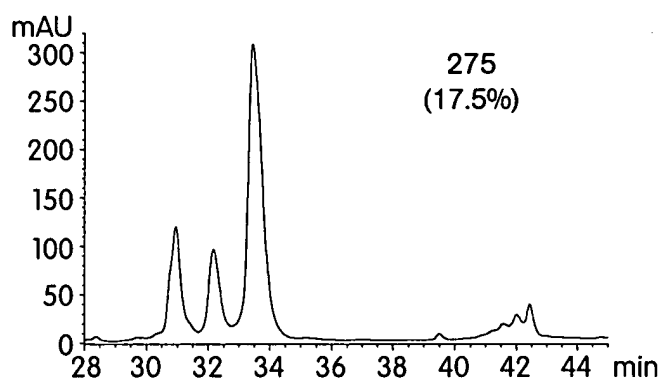


Fig. 15F

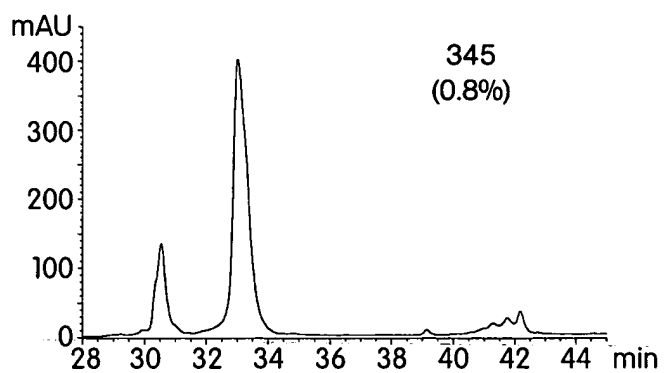


Fig. 15G

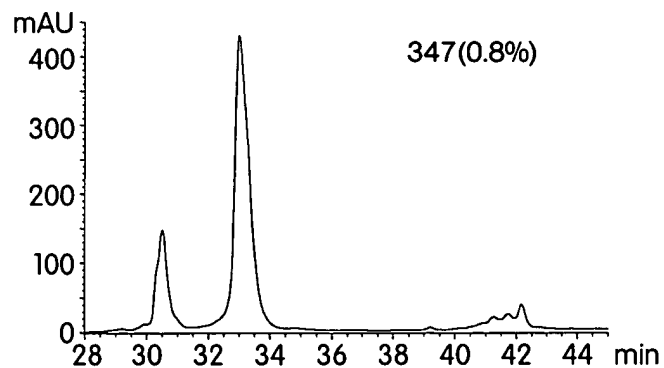
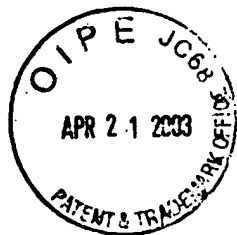


Fig. 15H



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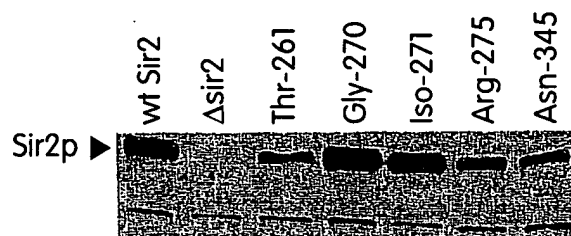


Fig. 16A

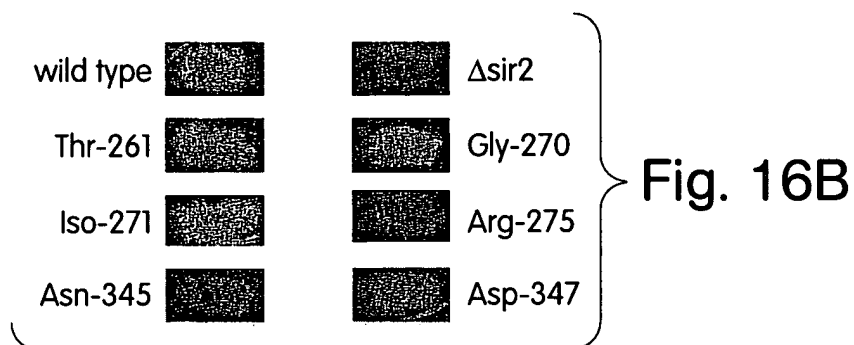


Fig. 16B

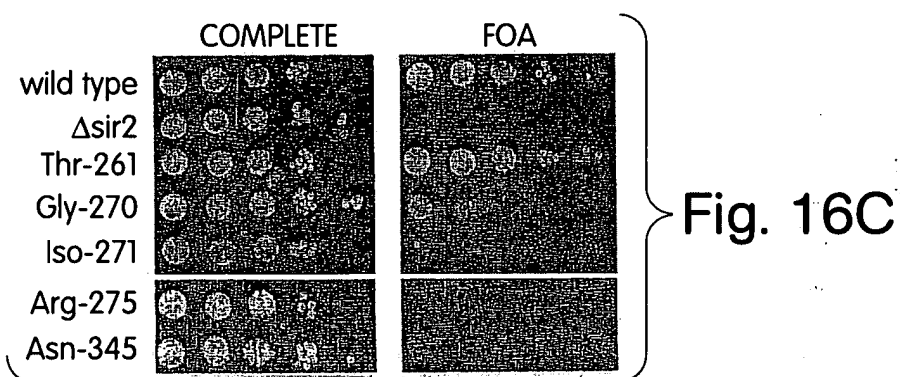


Fig. 16C

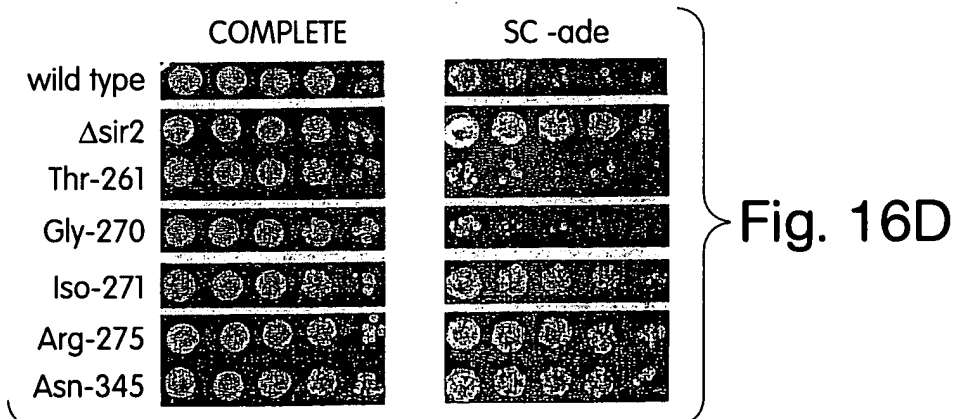
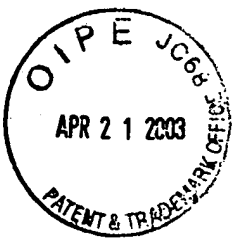


Fig. 16D



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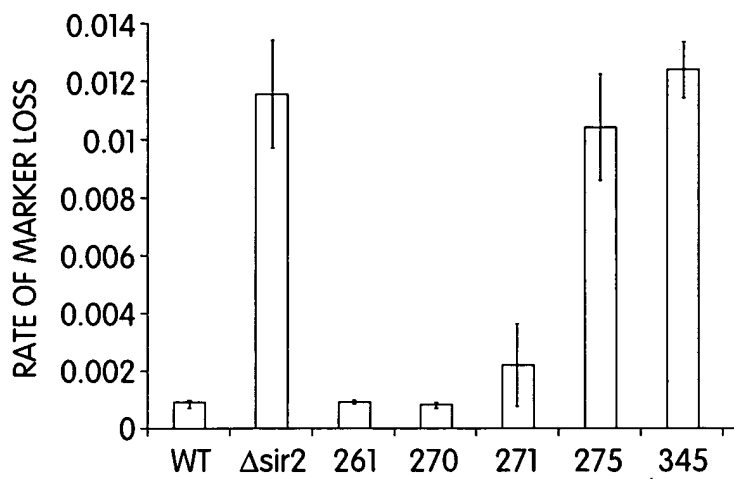


Fig. 17A

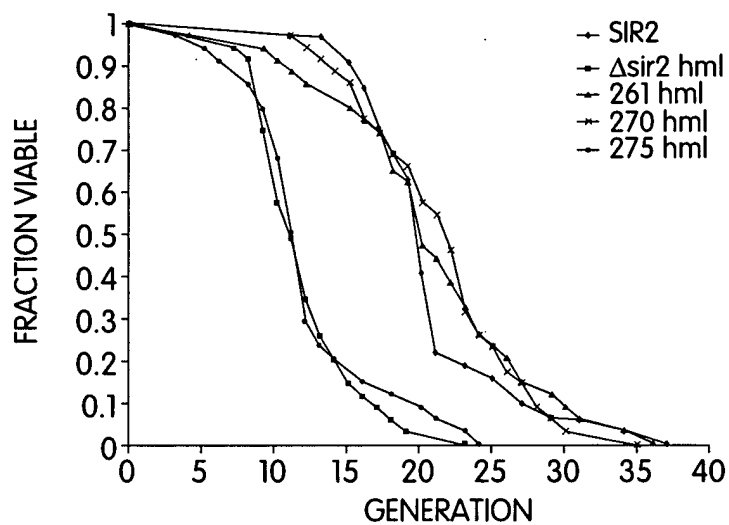


Fig. 17B

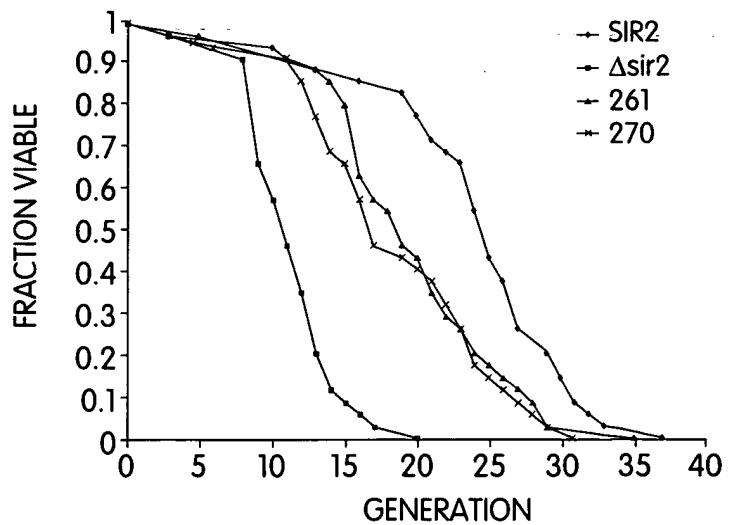


Fig. 17C



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Mutant	ADP-Rib. Activity (% of wt)	Deacetylase Activity (% of wt)	HM Silencing	Telomere Silencing	rDNA Silencing	rDNA Recombi- nation	Mean Life Span (HML+)
sir2Δ	0%	2.7%	-	-	-	1.15%	11.4
wildtype	100%	100%	+	+	+	0.09%	24.4
Thr-261	4%	17%	+	+	+	0.09%	19.8
Gly-270	7%	80%	+	+/-	+	0.08%	18.9
Iso-271	8%	36%	+	-	+/-	0.22%	ND
Arg-275	100%	67%	-	-	-	1.03%	ND
Arg-345	0%	3%	-	-	-	1.22%	ND
Asp-347	0%	3%	-	ND	ND	ND	ND

Fig. 18



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ySIR2	257	TLVLTGAGVSTSLGIPDFRS	-SEGFYSKIKH	--	286
yHST1	203	TLVLTGAGVSTSLGIPDFRS	-SEGFYSKIRH	--	232
yHST2	27	VIFMVGAGISTSCGIPDFRS	PGTGGLYHNLAR	--	57
yHST3	55	IACLTGAGISTCNAGIPDFRS	-SDGLYDLVKDC	86	
yHST4	95	MVVVSGAGISVAAGIPDFRS	-SEGIFSTVNGGS	126	
mSIR2alpha	263	IIVLTGAGVSVSCGIPDFRS	-RDGIYARLAVDF	294	
mSIR2beta	79	VICLVGAGISTSAAGIPDFRS	PSGTGLYANLEK	--	109
mSIR2g...	1	-----	-GTRLYSNLQQ	--	10
AI465098	48	VVFHTGAGISTASGIPDFRG	-PHGVWTMEER	--	77
AI465820	67	LLVMTGAGISTESGIPDYRSE	EKVGLYARTDR	--	97
AI466061	59	IATISGAGVSAESGVPTFRG	-AGGYWRKWQA	--	88
ySIR2	287	---LGLDDPQDVFNYNIFMHDP	SV---FYNIANM	314	
yHST1	233	---LGLDDPQDVFNLDIFLQDP	SV---FYNIAHM	260	
yHST2	58	---LKLPYPEAVFDVDFQSDPLP	---FYT LAKE	85	
yHST3	87	SQYWSIKSGREMFDISLFRDDFK	TSIFA KFMER	119	
yHST4	127	---GKDLFDYNRVYGD ESM	SLKFN---QLMVSLE	154	
mSIR2alpha	295	---PDLPPDQAMFDIEYERKDRP	---FFKFAKE	322	
mSIR2beta	110	---YHLPYPEAIF EISYFKKH	PEP---FFALAKE	137	
mSIR2g...	11	---YDLPYPEAIFELGFFFHNP	KP---FFMLAKE	38	
AI465098	78	---GLAPKFDTTENA	-----	90	
AI465820	98	---RPIQ---HIDFVPVLR	SASG-----	114	
AI466061	89	---QDLATPQAFARNPSQVW	EYH-----YRRE	113	
ySIR2	315	VLP---PEKITYSPLHSFIKMLQ	MKGKLLLRN	NYTON	345
yHST1	261	VLP---PENMYSPLHSFIKMLQ	DKGKLLLRN	NYTON	291
yHST2	86	LVP---GNFRPSKPFHYLLKLFQ	DKDVLKR	VYTON	116
yHST3	120	LYSNVQLAKPTKTHKFI AHL	KDRNKL	LRCYTON	152
yHST4	155	RLS---KNCQPTKFHEMLNEF	ARDGRLL	RLRYTON	185
mSIR2alpha	323	LVP---GQFGPSLCHKFI ALS	DKEGKLL	LRNYTON	353
mSIR2beta	138	LVP---GQFKPTICHYFI RLL	KEKGL	LLRCYTON	168
mSIR2g...	39	LVP---GHYRPNVTHYFI RLL	HDKEL	LLRLYTON	69
AI465098	91	---R---PSKTHMALVQLERM	GFLSFLV	SON	115
AI465820	115	TWP---ENLWAGLNSPLINPT	OHTWL	-----	137
AI466061	114	VMR---SK-EPNPGHLAIAQ	CEAR	-----	133
ySIR2	346	IDNLESYAGISTD	-----KLVO	362	
yHST1	292	IDNLESYAGIDPD	-----KLVO	308	
yHST2	117	IDTLERQAGVKDD	-----LIIE	133	
yHST3	153	IDGLEESIGLTLSEN RK	LPLTSFSSH	WKNLDVVO	185
yHST4	186	IDGLDTQLPHLSTN	-----VPLAK	PIPSTVO	211
mSIR2alpha	354	IDTLEQVAGIQR	-----ILO	368	
mSIR2beta	169	IDTLERVAGLERQ	-----DLVE	185	
mSIR2g...	70	IDGLERASGIPAS	-----KLVE	86	
AI465098	116	VDGLDVRSGFPRD	-----KLAE	132	
AI465820	0	-----	-----	137	
AI466061	0	-----	-----	133	

Fig. 19

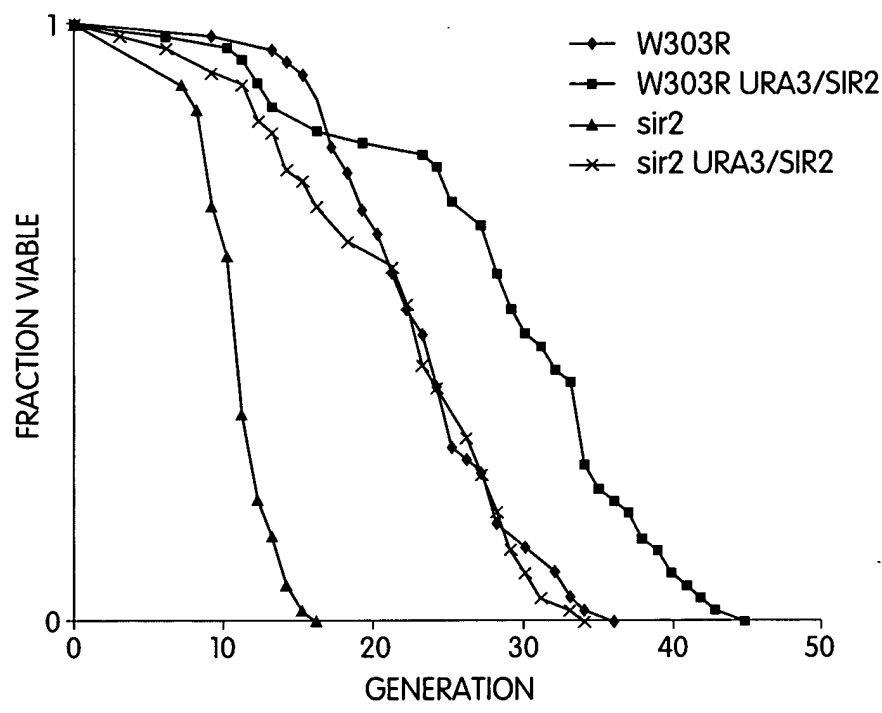


Fig. 20



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10 20 30 40 50 60
GCGGAGCAGAGGAGGCGAGGGCGAGGGCCAGAGAGGCAGTTGGAAGATGGCGGACGAGG
M A D E V

70 80 90 100 110 120
TGGCGCTCGCCCTTCAGGCCGCCGGCTCCCCTTCCGCGCGGCCGCCATGGAGGCCGCGT
A L A L Q A A G S P S A A A A M E A A S

130 140 150 160 170 180
CGCAGCCGGCGGACGAGCCGCTCCGCAAGAGGCCCCGCCGAGACGGGCCTGGCCTCGGGC
Q P A D E P L R K R P R R D G P G L G R

190 200 210 220 230 240
GCAGCCCGGGCGAGCCGAGCGCAGCAGTGGCGCCGGCGGCCGCGGGGTGTGAGGCGGCGA
S P G E P S A A V A P A A A G C E A A S

250 260 270 280 290 300
GCGCCGCGGCCCGCGGCGCTGTGGCGGGAGGCGGCAGGGGCGGCGGCGAGCGCGGAGC
A A A P A A L W R E A A G A A A S A E R

310 320 330 340 350 360
GGGAGGCCCCGCGACGCGCCGTGGCCGGGGACGGAGACAATGGGTCCGGCCTGCGGCGGG
E A P A T A V A G D G D N G S G L R R E

370 380 390 400 410 420
AGCCGAGGGCGGCTGACGACTTCGACGACGACGAGGGCGAGGAGGAGGACGAGGCGGCGG
P R A A D D F D D D E G E E E D E A A A

430 440 450 460 470 480
CGGCAGCGGCGGCGGCGAGCGATCGGCTACCGAGACAACCTCCTGTTGACCGATGGACTCC
A A A A A A I G Y R D N L L L T D G L L

490 500 510 520 530 540
TCACTAATGGCTTTTCATTCTGTGAAAGTGATGACGATGACAGAACGTCACACGCCAGCT
T N G F H S C E S D D D D R T S H A S S

550 560 570 580 590 600
CTAGTGACTGGACTCCGCGGCCCGGATAGGTCCATATACTTTTGTTCAGCAACATCTCA
S D W T P R P R I G P Y T F V Q Q H L M

610 620 630 640 650 660
TGATTGGCACCAGATCCTCGAACAATTCTTAAAGATTATTACCAGAAACAATTCCTCCAC
I G T D P R T I L K D L L P E T I P P P

670 680 690 700 710 720
CTGAGCTGGATGATATGACGCTGTGGCAGATTGTTATTAATATCCTTTTCAGAACCACCAA
E L D D M T L W Q I V I N I L S E P P K

730 740 750 760 770 780
AGCGGAAAAAAGAAAAGATATCAATACAATTGAAGATGCTGTGAAGTTACTGCAGGAGT
R K K R K D I N T I E D A V K L L Q E C

790 800 810 820 830 840
GTAAAAAGATAATAGTTCTGACTGGAGCTGGGGTTTCTGTCTCCTGTGGGATTCTGACT
K K I I V L T G A G V S V S C G I P D F

850 860 870 880 890 900
TCAGATCAAGAGACGGTATCTATGCTCGCCTTGCGGTGGACTTCCCAGACCTCCCAGACC
R S R D G I Y A R L A V D F P D L P D P

Fig. 21A



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910 920 930 940 950 960
CTCAAGCCATGTTTGATATTGAGTATTTTAGAAAAAGACCCAAGACCATTCTTCAAGTTTG
Q A M F D I E Y F R K D P R P F F K F A

970 980 990 1000 1010 1020
CAAAGGAAATATATCCCGGACAGTTCCAGCCGTCTCTGTGTACAAATTCATAGCTTTGT
K E I Y P G Q F Q P S L C H K F I A L S

1030 1040 1050 1060 1070 1080
CAGATAAGGAAGGAAACTACTTCGAAATTATACTCAAAATATAGATACCTTGGAGCAGG
D K E G K L L R N Y T Q N I D T L E Q V

1090 1100 1110 1120 1130 1140
TTGCAGGAATCCAAAGGATCCTTCAGTGTTCATGGTTCCTTTGCAACAGCATCTTGCCTGA
A G I Q R I L Q C H G S F A T A S C L I

1150 1160 1170 1180 1190 1200
TTTGTAATAACAAAGTTGATTGTGAAGCTGTTTCGTGGAGACATTTTTAATCAGGTAGTTC
C K Y K V D C E A V R G D I F N Q V V P

1210 1220 1230 1240 1250 1260
CTCGGTGCCCTAGGTGCCAGCTGATGAGCCACTTGCCATCATGAAGCCAGAGATTGTCT
R C P R C P A D E P L A I M K P E I V F

1270 1280 1290 1300 1310 1320
TCTTTGGTGAAAACCTTACCAGAACAGTTTCATAGAGCCATGAAGTATGACAAAGATGAAG
F G E N L P E Q F H R A M K Y D K D E V

1330 1340 1350 1360 1370 1380
TTGACCTCCTCATTGTTATTGGATCTTCTCTGAAAAGTGAGACCAGTAGCACTAATTCCAA
D L L I V I G S S L K V R P V A L I P S

1390 1400 1410 1420 1430 1440
GTTCTATACCCCATGAAGTGCCTCAAATATTAATAAATAGGGAACCTTTGCCTCATCTAC
S I P H E V P Q I L I N R E P L P H L H

1450 1460 1470 1480 1490 1500
ATTTTGATGTAGAGCTCCTTGGAGACTGCGATGTTATAATTAATGAGTTGTGTTCATAGGC
F D V E L L G D C D V I I N E L C H R L

1510 1520 1530 1540 1550 1560
TAGGTGGTGAATATGCCAAACTTTGTTGTAACCCTGTAAAGCTTTTCAGAAATTACTGAAA
G G E Y A K L C C N P V K L S E I T E K

1570 1580 1590 1600 1610 1620
AACCTCCACGCCCACAAAAGGAATTGGTTCAATTATCAGAGTTGCCACCAACACCTCTTC
P P R P Q K E L V H L S E L P P T P L H

1630 1640 1650 1660 1670 1680
ATATTTTCGGAAGACTCAAGTTCACCTGAAAGAACTGTACCACAAGACTCTTCTGTGATTG
I S E D S S S P E R T V P Q D S S V I A

1690 1700 1710 1720 1730 1740
CTACACTTGTAGACCAAGCAACAAACAACATGTTAATGATTTAGAAGTATCTGAATCAA
T L V D Q A T N N N V N D L E V S E S S

Fig. 21B



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1750 1760 1770 1780 1790 1800
GTTGTGTGGAAGAAAAACCACAAGAAGTACAGACTAGTAGGAATGTTGAGAACATTAATG
C V E E K P Q E V Q T S R N V E N I N V

1810 1820 1830 1840 1850 1860
TGGAAAATCCAGATTTTAAGGCTGTTGGTTCCAGTACTGCAGACAAAAATGAAAGAACTT
E N P D F K A V G S S T A D K N E R T S

1870 1880 1890 1900 1910 1920
CAGTTGCAGAAACAGTGAGAAAATGCTGGCCTAATAGACTTGCAAAGGAGCAGATTAGTA
V A E T V R K C W P N R L A K E Q I S K

1930 1940 1950 1960 1970 1980
AGCGGCTTGAGGGTAATCAATACCTGTTTGTACCACCAAATCGTTACATATTCCACGGTG
R L E G N Q Y L F V P P N R Y I F H G A

1990 2000 2010 2020 2030 2040
CTGAGGTATACTCAGACTCTGAAGATGACGTCTTGTCTCTAGTTCCTGTGGCAGTAACA
E V Y S D S E D D V L S S S S C G S N S

2050 2060 2070 2080 2090 2100
GTGACAGTGGCACATGCCAGAGTCCAAGTTTAGAAGAACCCTTGGAAGATGAAAGTGAAA
D S G T C Q S P S L E E P L E D E S E I

2110 2120 2130 2140 2150 2160
TTGAAGAATTCTACAATGGCTTGGAAGATGATACGGAGAGGCCCGAATGTGCTGGAGGAT
E E F Y N G L E D D T E R P E C A G G S

2170 2180 2190 2200 2210 2220
CTGGATTGAGCTGATGGAGGGGATCAAGAGGTTGTTAATGAAGCTATAGCTACAAGAC
G F G A D G G D Q E V V N E A I A T R Q

2230 2240 2250 2260 2270 2280
AGGAATTGACAGATGTAACTATCCATCAGACAAATCATAACACTATTGAAGCTGTCCGG
E L T D V N Y P S D K S *

2290 2300 2310 2320 2330 2340
ATTCAGGAATTGCTCCACCAGCATTGGGAACTTTAGCATGTCAAAAAAATGAATGTTTAC

2350 2360 2370 2380 2390 2400
TTGTGAACTTGAACAAGGAAATCTGAAAGATGTATTATTTATAGACTGGAAAATAGATTG

2410 2420 2430 2440 2450 2460
TCTTCTTGATAATTTCTAAAGTTCATCATTTCTGTTTGTACTTGTACATTCAACACTG

2470 2480 2490 2500 2510 2520
TTGGTTGACTTCATCTTCCTTTCAAGGTTCAATTTGTATGATACATTTCGTATGTATGTATA

2530 2540 2550 2560 2570 2580
ATTTTGTTTTTTGCCTAATGAGTTTCAACCTTTTAAAGTTTTTCAAAGCCATTGGAATGT

2590 2600 2610 2620 2630 2640
TAATGTAAAGGGAACAGCTTATCTAGACCAAAGAATGGTATTTTCACTTTTTTGTGTTGT

2650 2660 2670 2680 2690 2700
AACATTGAATAGTTTAAAGCCCTCAATTTCTGTTCTGCTGAACTTTTATTTTATAGGACAG

Fig. 21C



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2710 2720 2730 2740 2750 2760
TTAACTTTTTTAAACACTGGCATTTCCTCCAAAACCTGTGGCAGCTAACTTTTTTAAAATCACA

2770 2780 2790 2800 2810 2820
GATGACTTGTAATGTGAGGAGTCAGCACCGTGTCTGGAGCACTCAAACCTGGGCTCAGT

2830 2840 2850 2860 2870 2880
GTGTGAAGCGTACTTACTGCATCGTTTTTGTACTTGCTGCAGACGTGGTAATGTCCAAAC

2890 2900 2910 2920 2930 2940
AGGCCCCCTGAGACTAATCTGATAAATGATTTGGAAATGTGTTTCAGTTGTTCTAGAAACA

2950 2960 2970 2980 2990 3000
ATAGTGCCTGTCTATATAGGTCCCCTTAGTTTGAATATTTGCCATTGTTTAATTAAATAC

3010 3020 3030 3040 3050 3060
CTATCACTGTGGTAGAGCCTGCATAGATCTTCACCACAAATACTGCCAAGATGTGAATAT

3070 3080 3090 3100 3110 3120
GCAAAGCCTTTCTGAATCTAATAATGGTACTTCTACTGGGGAGAGTGTAATATTTTGGAC

3130 3140 3150 3160 3170 3180
TGCTGTTTTTCCATTAATGAGGAAAGCAATAGGCCTCTTAATTAAAGTCCCAAAGTCATA

3190 3200 3210 3220 3230 3240
AGATAAATTGTAGCTCAACCAGAAAGTACACTGTTGCCTGTTGAGGATTTGGTGTAATGT

3250 3260 3270 3280 3290 3300
ATCCCAAGGTGTTAGCCTTGTATTATGGAGATGAATACAGATCCAATAGTCAAATGAAAC

3310 3320 3330 3340 3350 3360
TAGTTCCTTAGTTATTTAAAAGCTTAGCTTGCCTTAAAACTAGGGATCAATTTCTCACT

3370 3380 3390 3400 3410 3420
GCAGAAACTTTTAGCCTTTCAAACAGTTCACACCTCAGAAAGTCAGTATTTATTTTACAG

3430 3440 3450 3460 3470 3480
ACTTCTTTGGAACATTGCCCCCAAATTTAAATATTCATGTGGGTTTAGTATTTATTACAA

3490 3500 3510 3520 3530 3540
AAAAATGATTTGAAATATAGCTGTTCTTTATGCATAAAATACCCAGTTAGGACCATTACT

3550 3560 3570 3580 3590 3600
GCCAGAGGAGAAAAGTATTAAGTAGCTCATTTCCCTACCTAAAAGATAACTGAATTTATT

3610 3620 3630 3640 3650 3660
TGGCTACACTAAAGAATGCAGTATATTTAGTTTTCCATTTGCATGATGTGTTTGTGCTAT

3670 3680 3690 3700 3710 3720
AGACAATATTTTAAATTGAAAAATTTGTTTTAAATTATTTTACAGTGAAGACTGTTTTTC

3730 3740 3750 3760 3770 3780
AGCTCTTTTTATATTGTACATAGACTTTTATGTAATCTGGCATATGTTTTGTAGACCGTT

3790 3800 3810 3820 3830 3840
TAATGACTGGATTATCTTCCTCCAACCTTTGAAATACAAAAACAGTGTTTTTATACTAAAA

3850 3860 3870
AAAAAAAAGTCGACGCGGCCGCGAATTC

Fig. 21D



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10 20 30 40 50 60
CCACGCGTCCGCGGACGCGTGGGCACGGGACAGAGCAGTCGGTGACAGTCCCCGAGGGCCC
T R P R T R G H G T E Q S V T V P R A P

70 80 90 100 110 120
CCACCCCGTTCCCATGGCCGAGCCGACCGATTTCAGACTCGGACACTGAGGGAGGAGCCA
T P F P W P S R T D S D S D T E G G A T

130 140 150 160 170 180
CTGGTGGAGAGGCAGAGATGGACTTCCTGAGGAATTTATTACCCAGACCCTGGGCCTGG
G G E A E M D F L R N L F T Q T L G L G

190 200 210 220 230 240
GTTCCCAAAAGGAGCGTCTTCTAGACGAGCTGACCCTCGAAGGAGTGACACGCTACATGC
S Q K E R L L D E L T L E G V T R Y M Q

250 260 270 280 290 300
AGAGCGAGCGCTGCCGCAAGGTCATCTGTTTGGTGGGAGCCGGAATCTCCACGTCCGCGG
S E R C R K V I C L V G A G I S T S A G

310 320 330 340 350 360
GTATCCCTGACTTCCGCTCCCCGTCCACTGGCCTCTATGCAAACCTGGAGAAGTACCACC
I P D F R S P S T G L Y A N L E K Y H L

370 380 390 400 410 420
TTCCTTACCCAGAGGCCATCTTTGAGATCAGCTACTTCAAGAAACATCCGGAACCCCTTCT
P Y P E A I F E I S Y F K K H P E P F F

430 440 450 460 470 480
TTGCCCTTGCCAAGGAGCTCTATCCCGGGCAGTTCAAGCCAACCATCTGCCACTACTTCA
A L A K E L Y P G Q F K P T I C H Y F I

490 500 510 520 530 540
TCCGCCTGCTGAAGGAGAAGGGGCTGCTGCTGCGCTGCTACACGCAGAACATAGACACGC
R L L K E K G L L L R C Y T Q N I D T L

550 560 570 580 590 600
TGGAACGAGTGGCGGGGCTGGAGCCCCAGGACCTGGTGGAGGCCACGGCACCTTCTACA
E R V A G L E P Q D L V E A H G T F Y T

610 620 630 640 650 660
CATCACACTGTGTCAACACCTCCTGCAGAAAAGAATACACGATGGGCTGGATGAAAGAGA
S H C V N T S C R K E Y T M G W M K E K

670 680 690 700
AGATTTCTCAGAAGCAACTCCCAGGTGTGAGCAGTGTCA
I S Q K Q L P G V S S V

Fig. 22